Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 08:30:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231860.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6231860 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231860.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 08:30:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231860.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,994,059
Mapped reads	1,432,889 / 71.86%
Unmapped reads	561,170 / 28.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,186 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	57,742 / 2.9%
Duplication rate	3.51%
Clipped reads	722,072 / 36.21%

2.2. ACGT Content

Number/percentage of A's	23,645,524 / 25.39%
Number/percentage of C's	18,714,077 / 20.09%
Number/percentage of T's	27,828,500 / 29.88%
Number/percentage of G's	22,939,389 / 24.63%
Number/percentage of N's	4,569 / 0%
GC Percentage	44.73%

2.3. Coverage

Mean	0.0301

Standard Deviation	0.2493

2.4. Mapping Quality

Mean Mapping Quality	39.68

2.5. Mismatches and indels

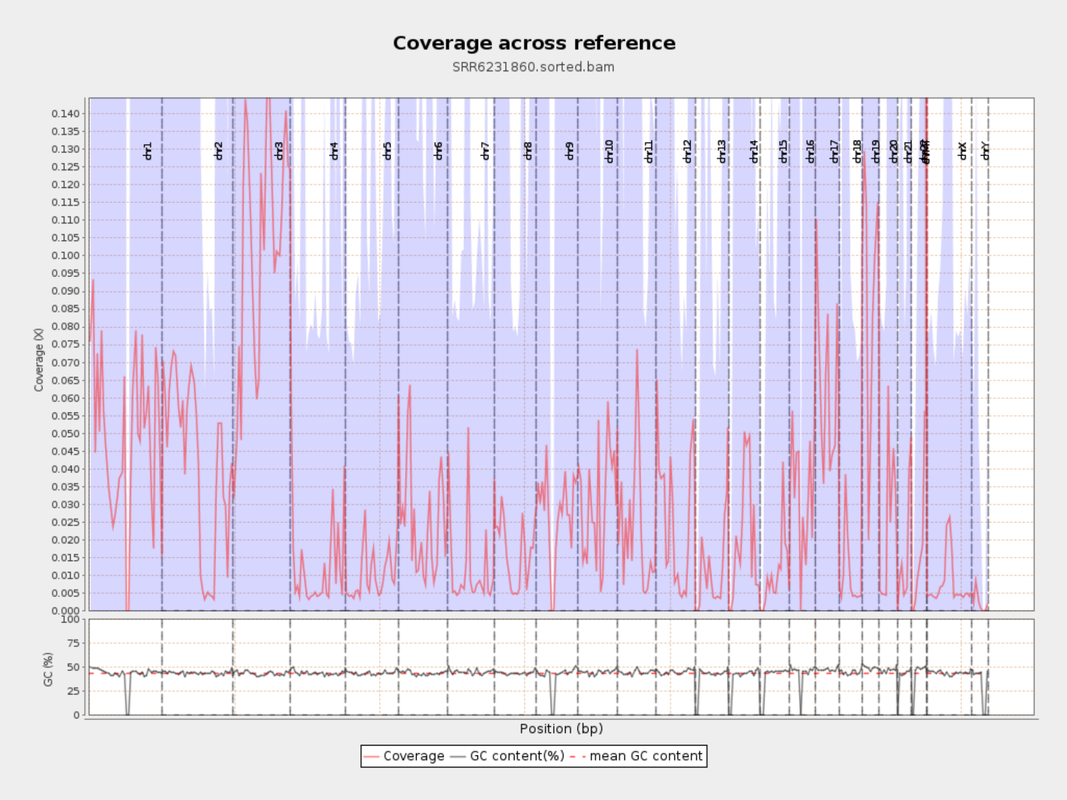
General error rate	0.71%
Mismatches	654,223
Insertions	5,955
Mapped reads with at least one insertion	0.41%
Deletions	24,107
Mapped reads with at least one deletion	1.66%
Homopolymer indels	44.08%

2.6. Chromosome stats

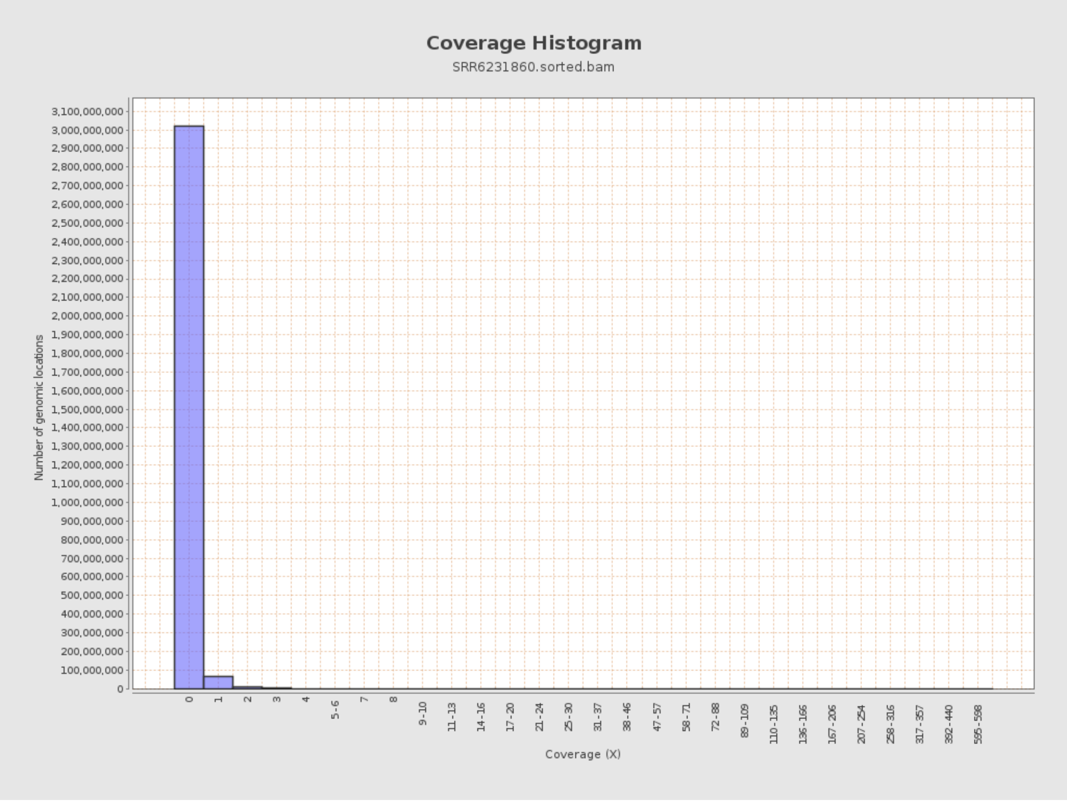
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12148032	0.0487	0.4418
chr2	243199373	10098465	0.0415	0.341
chr3	198022430	20320462	0.1026	0.3788
chr4	191154276	2351320	0.0123	0.1301
chr5	180915260	1820872	0.0101	0.1142
chr6	171115067	4429848	0.0259	0.2089
chr7	159138663	1817757	0.0114	0.1268

chr8	146364022	2340948	0.016	0.1539
chr9	141213431	3781396	0.0268	0.1933
chr10	135534747	4052019	0.0299	0.3144
chr11	135006516	3168423	0.0235	0.1842
chr12	133851895	3447169	0.0258	0.1886
chr13	115169878	1296236	0.0113	0.1248
chr14	107349540	2174892	0.0203	0.1671
chr15	102531392	1104061	0.0108	0.1219
chr16	90354753	3035922	0.0336	0.2157
chr17	81195210	5238520	0.0645	0.3077
chr18	78077248	784312	0.01	0.1462
chr19	59128983	5194673	0.0879	0.4414
chr20	63025520	1506163	0.0239	0.1801
chr21	48129895	806728	0.0168	0.1534
chr22	51304566	896592	0.0175	0.1534
chrMT	16571	53934	3.2547	2.5887
chrX	155270560	1163373	0.0075	0.1042
chrY	59373566	141830	0.0024	0.066

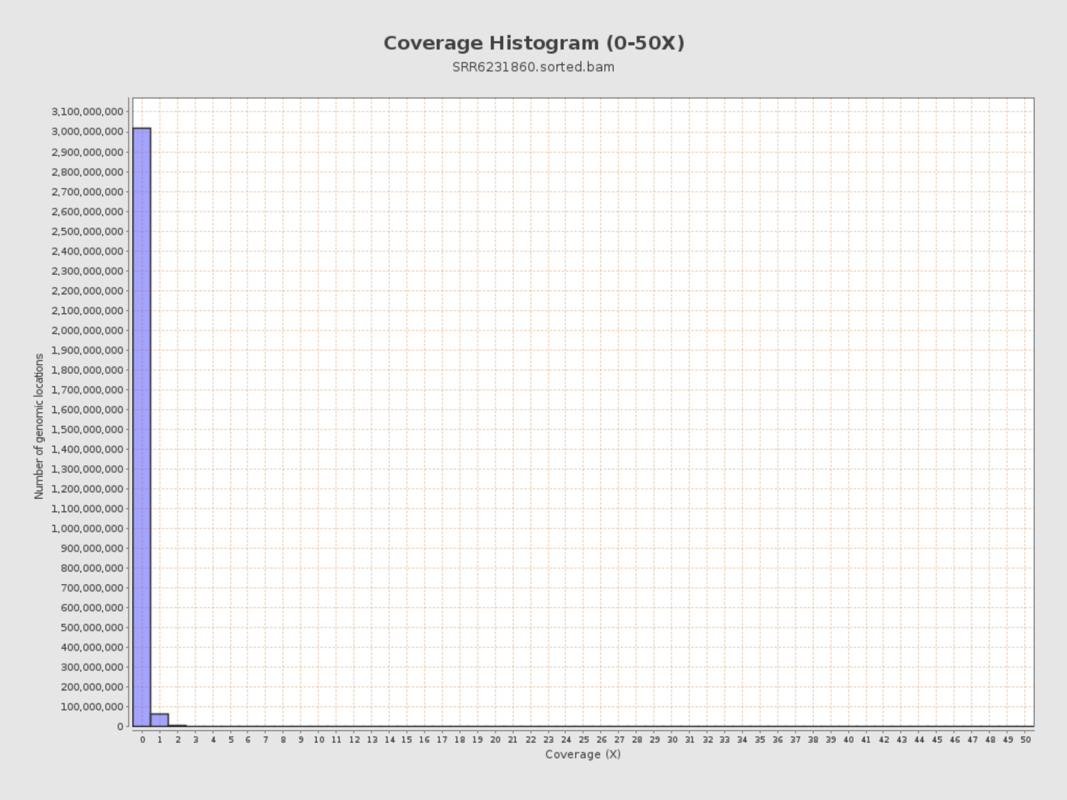
3. Results : Coverage across reference



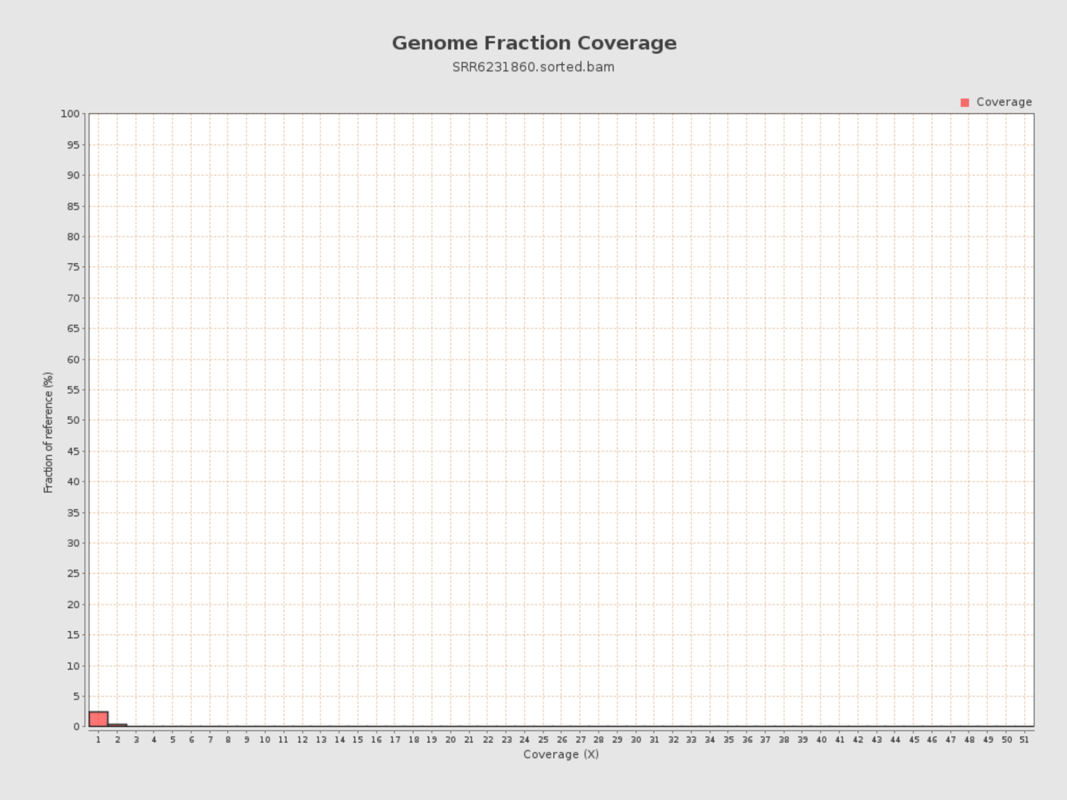
4. Results : Coverage Histogram



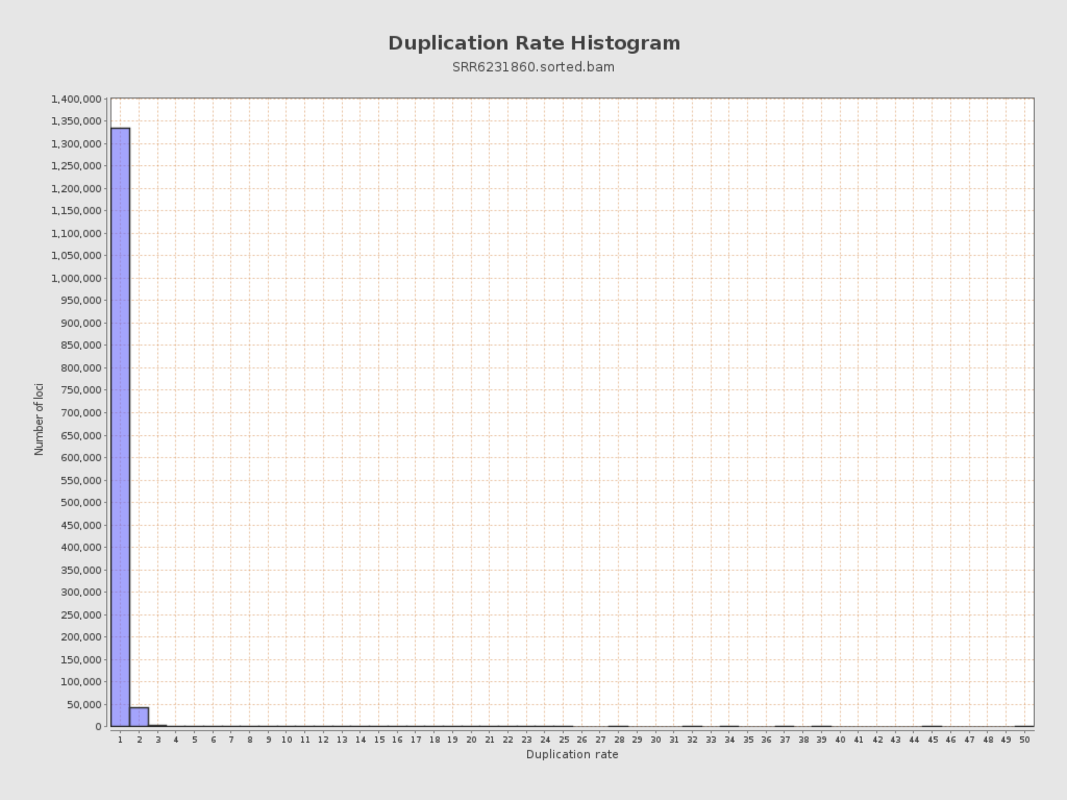
5. Results : Coverage Histogram (0-50X)



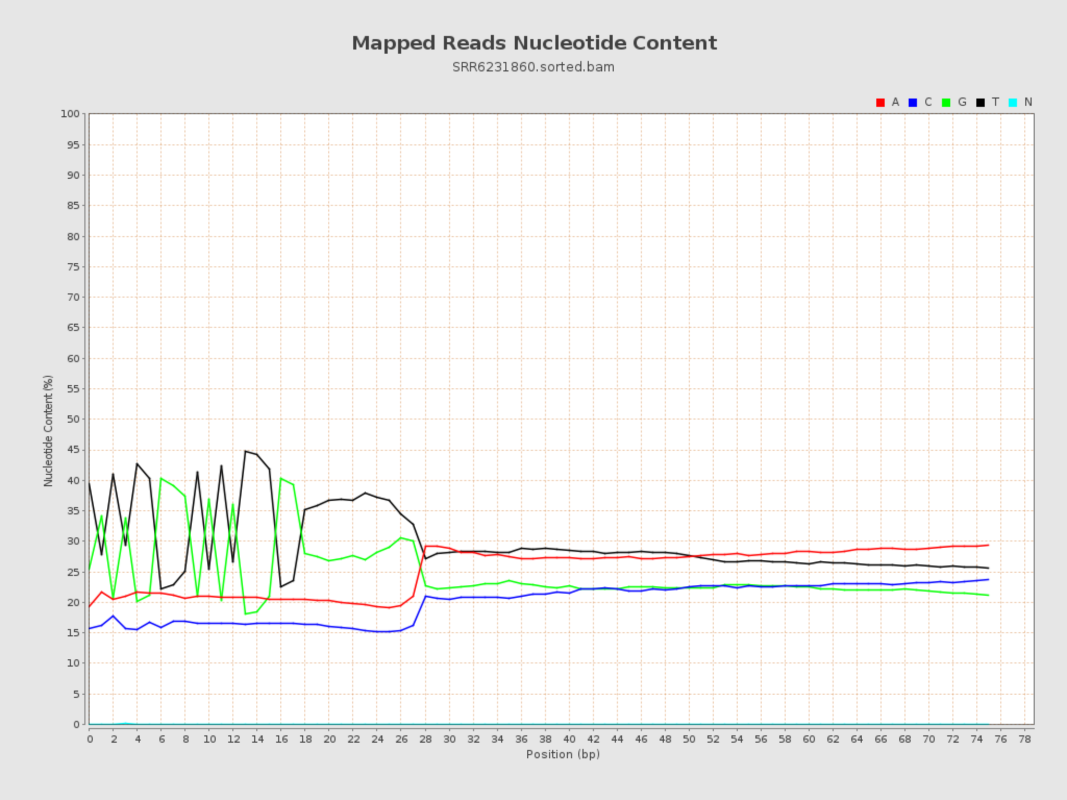
6. Results : Genome Fraction Coverage



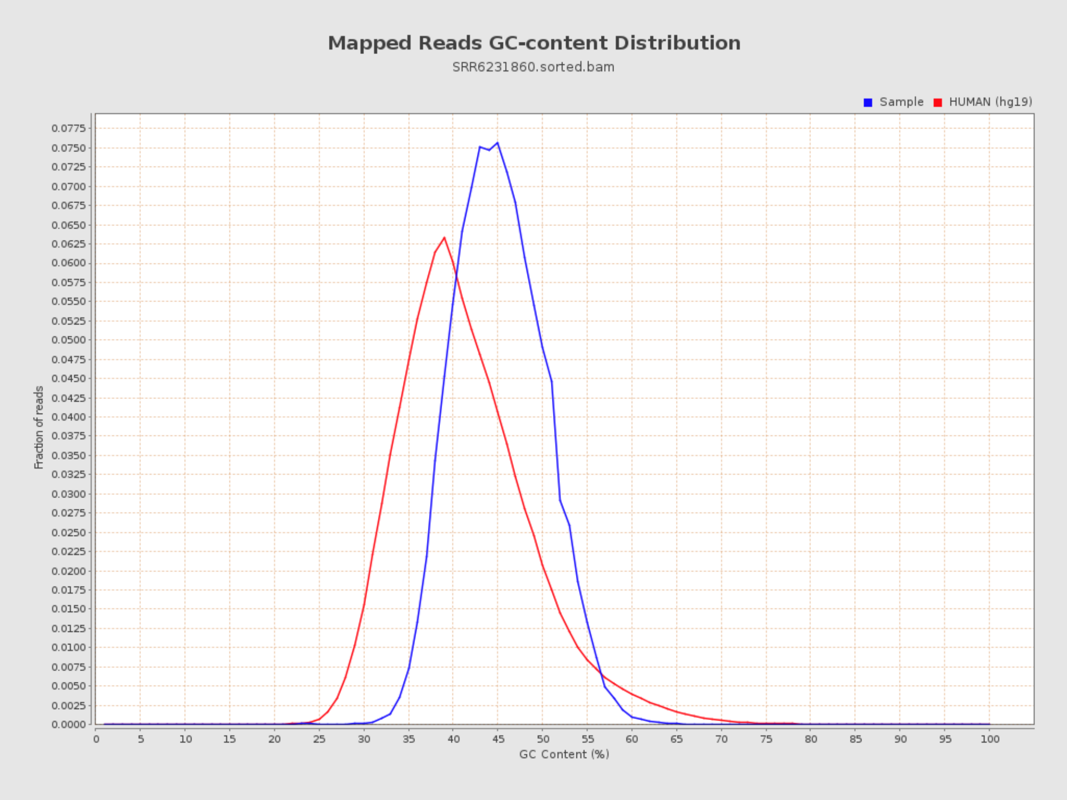
7. Results : Duplication Rate Histogram



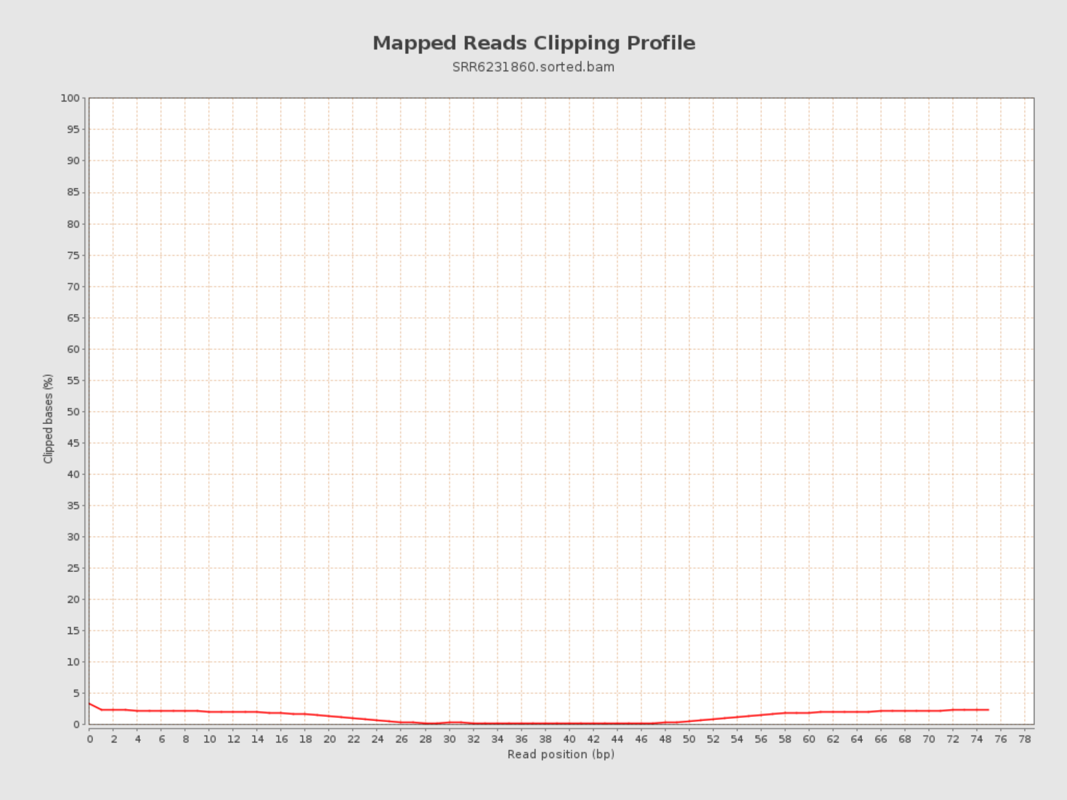
8. Results : Mapped Reads Nucleotide Content



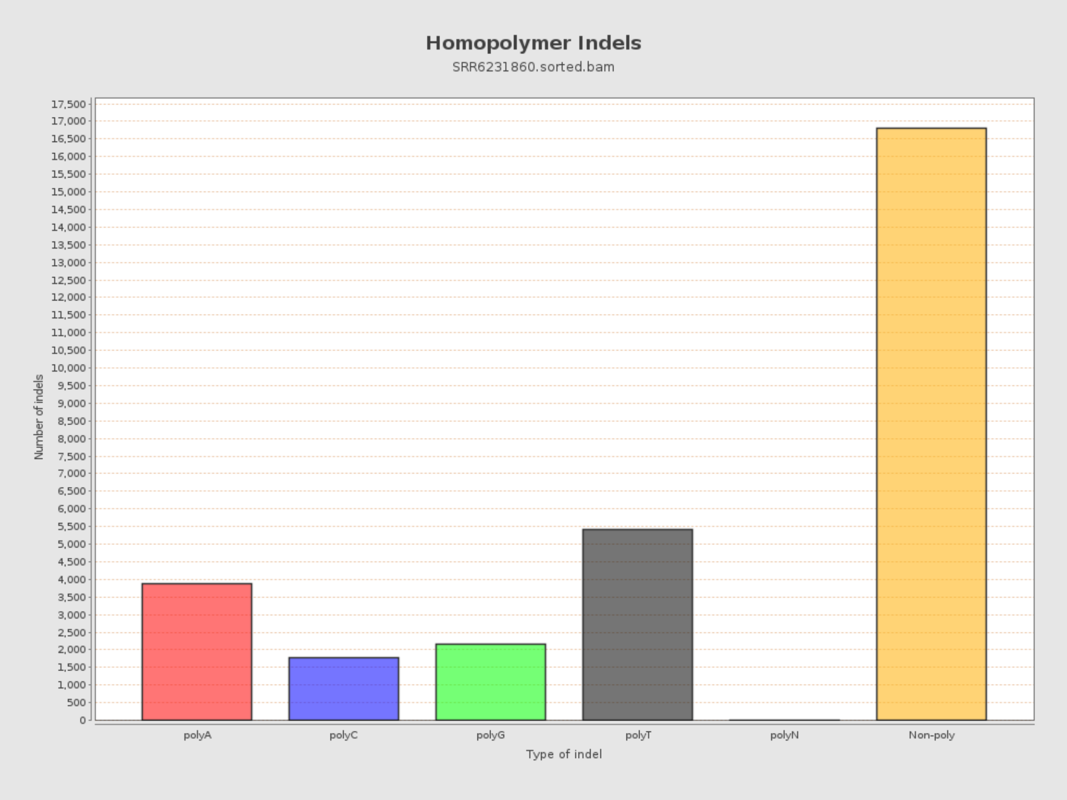
9. Results : Mapped Reads GC-content Distribution



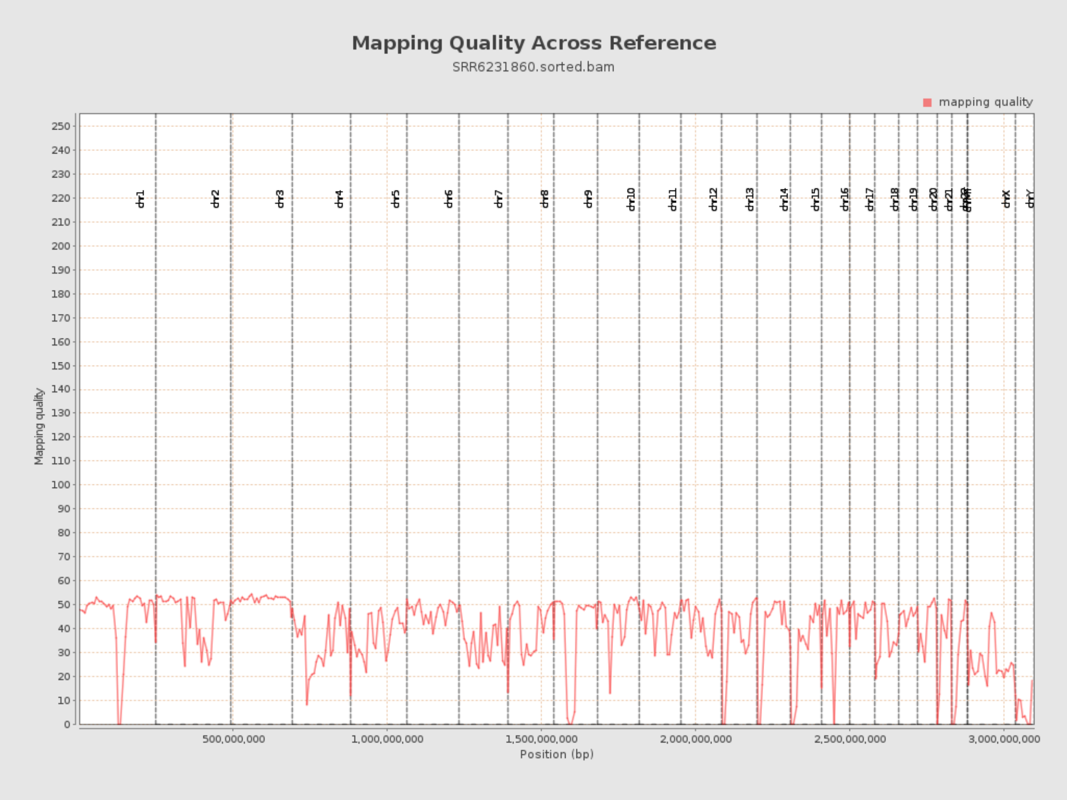
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram